

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number:

10/680,963A

Source:

IFWO

Date Processed by STIC:

5-26-05

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RAW SEQUENCE LISTING

DATE: 05/26/2005

PATENT APPLICATION: US/10/680,963A

TIME: 10:30:14

Input Set : A:\GFI-108 Sequence listing.ST25

Output Set: N:\CRF4\05262005\J680963A.raw

3 <110> APPLICANT: GlycoFi, Inc.
 4 Bobrowicz, Piotr
 5 Hamilton, Stephen R.
 6 Gerngross, Tilman U.
 7 Wildt, Stefan
 8 Choi, Byung-Kwon
 9 Nett, Juergen H.
 10 Davidson, Robert C.
 12 <120> TITLE OF INVENTION: N-Acetylglucosaminyltransferase III expression in lower
 13 eukaryotes
 15 <130> FILE REFERENCE: GFI-108 CIP
 17 <140> CURRENT APPLICATION NUMBER: US 10/680,963A
 18 <141> CURRENT FILING DATE: 2003-10-07
 20 <150> PRIOR APPLICATION NUMBER: US 10/371,877
 21 <151> PRIOR FILING DATE: 2003-02-20
 23 <150> PRIOR APPLICATION NUMBER: US 09/892,591
 24 <151> PRIOR FILING DATE: 2001-06-27
 26 <150> PRIOR APPLICATION NUMBER: US 60/214,358
 27 <151> PRIOR FILING DATE: 2000-06-28
 29 <150> PRIOR APPLICATION NUMBER: US 60/215,638
 30 <151> PRIOR FILING DATE: 2000-06-30
 32 <150> PRIOR APPLICATION NUMBER: US 60/279,997
 33 <151> PRIOR FILING DATE: 2001-03-30
 35 <150> PRIOR APPLICATION NUMBER: PCT/US02/41510
 36 <151> PRIOR FILING DATE: 2002-12-24
 38 <150> PRIOR APPLICATION NUMBER: US 60/344,169
 39 <151> PRIOR FILING DATE: 2001-12-27
 41 <160> NUMBER OF SEQ ID NOS: 101
 43 <170> SOFTWARE: PatentIn version 3.2
 45 <210> SEQ ID NO: 1
 W--> 46 <400> SEQUENCE: 1
 W--> 47 000
 50 <210> SEQ ID NO: 2
 W--> 51 <400> SEQUENCE: 2
 W--> 52 000
 55 <210> SEQ ID NO: 3
 56 <211> LENGTH: 21
 57 <212> TYPE: DNA
 58 <213> ORGANISM: artificial
 60 <220> FEATURE:
 61 <223> OTHER INFORMATION: Primer A for target gene in P. pastoris (1,6-
 mannosyltransferase)
 63 <400> SEQUENCE: 3
 64 atggcgaagg cagatggcag t

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67 <210> SEQ ID NO: 4
68 <211> LENGTH: 21
69 <212> TYPE: DNA
70 <213> ORGANISM: artificial
72 <220> FEATURE:
73 <223> OTHER INFORMATION: Primer B for target gene in P. pastoris (1,6-
mannosyltransferase)
75 <400> SEQUENCE: 4
76 ttagtccttc caacttcctt c                               21
79 <210> SEQ ID NO: 5
80 <211> LENGTH: 26
81 <212> TYPE: DNA
82 <213> ORGANISM: artificial
84 <220> FEATURE:
85 <223> OTHER INFORMATION: Primer A for target gene in P. pastoris (1,2
86     mannosyltransferases)
89 <220> FEATURE:
90 <221> NAME/KEY: misc_feature
91 <222> LOCATION: (9)..(9)
92 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
94 <220> FEATURE:
95 <221> NAME/KEY: misc_feature
96 <222> LOCATION: (12)..(12)
97 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
99 <220> FEATURE:
100 <221> NAME/KEY: misc_feature
101 <222> LOCATION: (18)..(18)
102 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
104 <400> SEQUENCE: 5
W--> 105 taytggmgng tngarcynga yathaa                      26
108 <210> SEQ ID NO: 6
109 <211> LENGTH: 20
110 <212> TYPE: DNA
111 <213> ORGANISM: artificial
113 <220> FEATURE:
114 <223> OTHER INFORMATION: Primer B for target gene in P. pastoris (1,2
115     mannosyltransferases)
118 <220> FEATURE:
119 <221> NAME/KEY: misc_feature
120 <222> LOCATION: (6)..(6)
121 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
123 <220> FEATURE:
124 <221> NAME/KEY: misc_feature
125 <222> LOCATION: (12)..(12)
126 <223> OTHER INFORMATION: wherein "n" is equal to "a" or "t" or "g" or "c".
128 <400> SEQUENCE: 6
W--> 129 gcrtncccc anckytcrta                              20
132 <210> SEQ ID NO: 7
W--> 133 <400> SEQUENCE: 7
W--> 134 000

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137 <210> SEQ ID NO: 8
W--> 138 <400> SEQUENCE: 8
W--> 139 000
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143 <211> LENGTH: 458
144 <212> TYPE: PRT
145 <213> ORGANISM: Saccharomyces cerevisiae
147 <400> SEQUENCE: 9
149 Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
150 1 5 10 15
153 Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
154 20 25 30
157 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
158 35 40 45
161 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Lys Lys
162 50 55 60
165 Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
166 65 70 75 80
169 Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
170 85 90 95
173 Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
174 100 105 110
177 Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
178 115 120 125
181 Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
182 130 135 140
185 Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
186 145 150 155 160
189 Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
190 165 170 175
193 Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
194 180 185 190
197 Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
198 195 200 205
201 Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu
202 210 215 220
205 Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
206 225 230 235 240
209 Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
210 245 250 255
213 Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
214 260 265 270
217 His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
218 275 280 285
221 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His
222 290 295 300
225 Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val
226 305 310 315 320
229 Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His

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230          325          330          335
233 Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
234          340          345          350
237 Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
238          355          360          365
241 Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
242          370          375          380
245 Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
246 385          390          395          400
249 Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala
250          405          410          415
253 Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Leu Ala
254          420          425          430
257 Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg
258          435          440          445
261 Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
262          450          455
265 <210> SEQ ID NO: 10
266 <211> LENGTH: 458
267 <212> TYPE: PRT
268 <213> ORGANISM: Saccharomyces cerevisiae
270 <400> SEQUENCE: 10
272 Met Glu Gly Glu Gln Ser Pro Gln Gly Glu Lys Ser Leu Gln Arg Lys
273 1          5          10          15
276 Gln Phe Val Arg Pro Pro Leu Asp Leu Trp Gln Asp Leu Lys Asp Gly
277          20          25          30
280 Val Arg Tyr Val Ile Phe Asp Cys Arg Ala Asn Leu Ile Val Met Pro
281          35          40          45
284 Leu Leu Ile Leu Phe Glu Ser Met Leu Cys Lys Ile Ile Ile Lys Lys
285          50          55          60
288 Val Ala Tyr Thr Glu Ile Asp Tyr Lys Ala Tyr Met Glu Gln Ile Glu
289 65          70          75          80
292 Met Ile Gln Leu Asp Gly Met Leu Asp Tyr Ser Gln Val Ser Gly Gly
293          85          90          95
296 Thr Gly Pro Leu Val Tyr Pro Ala Gly His Val Leu Ile Tyr Lys Met
297          100         105         110
300 Met Tyr Trp Leu Thr Glu Gly Met Asp His Val Glu Arg Gly Gln Val
301          115         120         125
304 Phe Phe Arg Tyr Leu Tyr Leu Leu Thr Leu Ala Leu Gln Met Ala Cys
305          130         135         140
308 Tyr Tyr Leu Leu His Leu Pro Pro Trp Cys Val Val Leu Ala Cys Leu
309 145         150         155         160
312 Ser Lys Arg Leu His Ser Ile Tyr Val Leu Arg Leu Phe Asn Asp Cys
313          165         170         175
316 Phe Thr Thr Leu Phe Met Val Val Thr Val Leu Gly Ala Ile Val Ala
317          180         185         190
320 Ser Arg Cys His Gln Arg Pro Lys Leu Lys Lys Ser Leu Ala Leu Val
321          195         200         205
324 Ile Ser Ala Thr Tyr Ser Met Ala Val Ser Ile Lys Met Asn Ala Leu

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```

325      210      215      220
328 Leu Tyr Phe Pro Ala Met Met Ile Ser Leu Phe Ile Leu Asn Asp Ala
329 225      230      235      240
332 Asn Val Ile Leu Thr Leu Leu Asp Leu Val Ala Met Ile Ala Trp Gln
333      245      250      255
336 Val Ala Val Ala Val Pro Phe Leu Arg Ser Phe Pro Gln Gln Tyr Leu
337      260      265      270
340 His Cys Ala Phe Asn Phe Gly Arg Lys Phe Met Tyr Gln Trp Ser Ile
341      275      280      285
344 Asn Trp Gln Met Met Asp Glu Glu Ala Phe Asn Asp Lys Arg Phe His
345      290      295      300
348 Leu Ala Leu Leu Ile Ser His Leu Ile Ala Leu Thr Thr Leu Phe Val
349 305      310      315      320
352 Thr Arg Tyr Pro Arg Ile Leu Pro Asp Leu Trp Ser Ser Leu Cys His
353      325      330      335
356 Pro Leu Arg Lys Asn Ala Val Leu Asn Ala Asn Pro Ala Lys Thr Ile
357      340      345      350
360 Pro Phe Val Leu Ile Ala Ser Asn Phe Ile Gly Val Leu Phe Ser Arg
361      355      360      365
364 Ser Leu His Tyr Gln Phe Leu Ser Trp Tyr His Trp Thr Leu Pro Ile
365      370      375      380
368 Leu Ile Phe Trp Ser Gly Met Pro Phe Phe Val Gly Pro Ile Trp Tyr
369 385      390      395      400
372 Val Leu His Glu Trp Cys Trp Asn Ser Tyr Pro Pro Asn Ser Gln Ala
373      405      410      415
376 Ser Thr Leu Leu Leu Ala Leu Asn Thr Val Leu Leu Leu Leu Leu Ala
377      420      425      430
380 Leu Thr Gln Leu Ser Gly Ser Val Ala Leu Ala Lys Ser His Leu Arg
381      435      440      445
384 Thr Thr Ser Ser Met Glu Lys Lys Leu Asn
385      450      455
388 <210> SEQ ID NO: 11
389 <211> LENGTH: 389
390 <212> TYPE: PRT
391 <213> ORGANISM: Saccharomyces cerevisiae
393 <400> SEQUENCE: 11
395 Trp Gln Asp Leu Lys Asp Gly Val Arg Tyr Val Ile Phe Asp Cys Arg
396 1      5      10      15
399 Ala Asn Leu Ile Val Met Pro Leu Leu Ile Leu Phe Glu Ser Met Leu
400      20      25      30
403 Cys Lys Ile Ile Ile Lys Lys Val Ala Tyr Thr Glu Ile Asp Tyr Lys
404      35      40      45
407 Ala Tyr Met Glu Gln Ile Glu Met Ile Gln Leu Asp Gly Met Leu Asp
408      50      55      60
411 Tyr Ser Gln Val Ser Gly Gly Thr Gly Pro Leu Val Tyr Pro Ala Gly
412 65      70      75      80
415 His Val Leu Ile Tyr Lys Met Met Tyr Trp Leu Thr Glu Gly Met Asp
416      85      90      95
419 His Val Glu Arg Gly Gln Val Phe Phe Arg Tyr Leu Tyr Leu Leu Thr

```

RAW SEQUENCE LISTING ERROR SUMMARY DATE: 05/26/2005
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:5; N Pos. 9,12,18 ✓

Seq#:6; N Pos. 6,12 ✓

Seq#:75; N Pos. 17,20

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete,
per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:3,4,5,6,41,42,47,48,49,52,53,54,55,56,57,58,59,60,61,62,63,64,65,66,67,68

Seq#:69,70,71,72,73,74,75,76,77,78,79,80,81,82,83,84,85,86,87,88,89,94,95,96

Seq#:97,98,99,100,101

VERIFICATION SUMMARY

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Input Set : A:\GFI-108 Sequence listing.ST25

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L:46 M:283 W: Missing Blank Line separator, <400> field identifier
L:47 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (1) SEQUENCE:
L:51 M:283 W: Missing Blank Line separator, <400> field identifier
L:52 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (2) SEQUENCE:
L:105 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:5 after pos.:0
L:129 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:6 after pos.:0
L:133 M:283 W: Missing Blank Line separator, <400> field identifier
L:134 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (7) SEQUENCE:
L:138 M:283 W: Missing Blank Line separator, <400> field identifier
L:139 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (8) SEQUENCE:
L:2445 M:283 W: Missing Blank Line separator, <400> field identifier
L:2446 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (43) SEQUENCE:
L:2450 M:283 W: Missing Blank Line separator, <400> field identifier
L:2451 M:300 W: (50) Intentionally skipped Sequence, : Sequence Id (44) SEQUENCE:
L:3240 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:75 after pos.:0